



#8

SEQUENCE LISTING

<110> Attersand, Anneli

<120> Protein Cluster II

<130> 10806-156

<140> 10/029,359

<141> 2001-12-21

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 299

<212> DNA

<213> HUMAN

<220>

<221> CDS

<222> (21)..(299)

<223>

B

<400> 1
gcaagagggga gccacggccg atg aca gaa aat tca ctt tcc gag atg gcc tct 53
Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser
1 5 10

aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg 101
Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly
15 20 25

ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt 149
Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly
30 35 40

gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca 197
Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser
45 50 55

gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca 245
Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala
60 65 70 75

gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc 293
 Asp Ser Ser Gln Arg Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu
 80 85 90

tat tag 299
 Tyr

<210> 2

<211> 92

<212> PRT

<213> HUMAN

<400> 2

Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser Lys Ser Trp Leu Asn
 1 5 10 15

Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly Phe Ile Leu Phe Ser
 20 25 30

Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
 35 40 45

Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
 50 55 60

Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
 65 70 75 80

Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr
 85 90

<210> 3

<211> 489

<212> DNA

<213> HUMAN

<220>

<221> CDS

<222> (55)..(489)

<223>

<400> 3

catctaaaaa gactgatgaa gttgattgca aatgctagtc atcataaata ccag aac
 Asn
 1

57

aca ggt gtc act gac aaa ctc tat caa aag atg aaa att ctt tgc tgg 105
 Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp
 5 10 15
 att atg aca gga cct caa aat cta gaa aaa aag atc aga cgc atc aga 153
 Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg
 20 25 30
 gat aca tgg gcc cag ggt tgc aat aaa gcg ttg ttt atg agc tca aaa 201
 Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser Lys
 35 40 45
 gaa aat aaa gac ttc tct act gtg gga tta cac acc aaa gaa gac aga 249
 Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp Arg
 50 55 60 65
 aac caa ctg tcc tgg aaa ata gtt aaa gct ttt cta tat gct cat gac 297
 Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp
 70 75 80
 cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata 345
 His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile
 85 90 95
 tgt ata tat atc aca ttg gac aac ttg aaa tgg ctt ctc aca aac tat 393
 Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr
 100 105 110
 aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga 441
 Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg
 115 120 125
 aaa cag gac tac atg act gga gga gca gga tat gta ctg agc aaa gaa 489
 Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu
 130 135 140 145

<210> 4
 <211> 145
 <212> PRT
 <213> HUMAN

<400> 4

Asn Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys
 1 5 10 15
 Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
 20 25 30
 Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
 35 40 45
 Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
 50 55 60
 Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
 65 70 75 80

Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
85 90 95

Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
100 105 110

Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
115 120 125

Arg Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys
130 135 140

Glu
145

<210> 5

<211> 1560

<212> DNA

<213> HUMAN

<220>

<221> CDS

<222> (2)..(934)

<223>

<400> 5

a gat aat gga cag aat cat cta gaa gga caa atg aac ttc aat gca gat 49
Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
1 5 10 15

tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat 97
Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
20 25 30

cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta 145
Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
35 40 45

gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac 193
Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60

aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg 241
Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80

gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att 289
Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95

aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg 337
Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
100 105 110

ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg 385

B'

Phe	Leu	Lys	Ala	Asp	Asp	Asp	Thr	Tyr	Val	Ile	Leu	Asp	Asn	Leu	Arg		
		115					120					125					
tgg	ctt	ctt	tca	aaa	tac	gac	cct	gaa	gaa	ccc	att	tac	ttt	ggg	aga	433	
Trp	Leu	Leu	Ser	Lys	Tyr	Asp	Pro	Glu	Glu	Pro	Ile	Tyr	Phe	Gly	Arg		
	130					135					140						
aga	ttt	aag	cct	tat	gta	aag	cag	ggc	tac	atg	agt	gga	gga	gca	gga	481	
Arg	Phe	Lys	Pro	Tyr	Val	Lys	Gln	Gly	Tyr	Met	Ser	Gly	Gly	Ala	Gly		
	145				150					155					160		
tat	gta	cta	agc	aaa	gaa	gcc	ttg	aaa	aga	ttt	gtt	gat	gca	ttt	aaa	529	
Tyr	Val	Leu	Ser	Lys	Glu	Ala	Leu	Lys	Arg	Phe	Val	Asp	Ala	Phe	Lys		
				165					170					175			
aca	gac	aag	tgt	aca	cat	agt	tcc	tcc	att	gaa	gac	tta	gca	ctg	ggg	577	
Thr	Asp	Lys	Cys	Thr	His	Ser	Ser	Ser	Ile	Glu	Asp	Leu	Ala	Leu	Gly		
			180					185					190				
aga	tgc	atg	gaa	att	atg	aat	gta	gaa	gca	gga	gat	tcc	aga	gat	acc	625	
Arg	Cys	Met	Glu	Ile	Met	Asn	Val	Glu	Ala	Gly	Asp	Ser	Arg	Asp	Thr		
		195					200					205					
att	gga	aaa	gaa	act	ttt	cat	ccc	ttt	gtg	cca	gaa	cac	cat	tta	att	673	
Ile	Gly	Lys	Glu	Thr	Phe	His	Pro	Phe	Val	Pro	Glu	His	His	Leu	Ile		
	210					215					220						
aaa	ggt	tat	cta	cct	aga	acg	ttt	tgg	tac	tgg	aat	tac	aac	tat	tat	721	
Lys	Gly	Tyr	Leu	Pro	Arg	Thr	Phe	Trp	Tyr	Trp	Asn	Tyr	Asn	Tyr	Tyr		
	225				230					235					240		
cct	cct	gta	gag	ggt	cct	ggt	tgc	tgc	tct	gat	ctt	gca	ggt	tct	ttt	769	
Pro	Pro	Val	Glu	Gly	Pro	Gly	Cys	Cys	Ser	Asp	Leu	Ala	Val	Ser	Phe		
				245					250					255			
cac	tat	ggt	gat	tct	aca	acc	atg	tat	gag	tta	gaa	tac	ctc	ggt	tat	817	
His	Tyr	Val	Asp	Ser	Thr	Thr	Met	Tyr	Glu	Leu	Glu	Tyr	Leu	Val	Tyr		
			260					265					270				
cat	ctt	cgt	cca	tat	ggt	tat	tta	tac	aga	tat	caa	cct	acc	tta	cct	865	
His	Leu	Arg	Pro	Tyr	Gly	Tyr	Leu	Tyr	Arg	Tyr	Gln	Pro	Thr	Leu	Pro		
		275					280					285					
gaa	cgt	ata	cta	aag	gaa	att	agt	caa	gca	aac	aaa	aat	gaa	gat	aca	913	
Glu	Arg	Ile	Leu	Lys	Glu	Ile	Ser	Gln	Ala	Asn	Lys	Asn	Glu	Asp	Thr		
	290					295					300						
aaa	gtg	aag	tta	gga	aat	cct	tgaaagaaaa	tc	atgaatga	acaaaggtaa						964	
Lys	Val	Lys	Leu	Gly	Asn	Pro											
	305				310												
tatgtctagc	actgcactga	aaaaggactt	ctgcatttct	gacatagaac	actggaatcc											1024	
cagtgaggaa	ttctaagtga	acattcctta	tagaaacctt	tcacatgaat	gactataaac											1084	
tgaagcttta	aatgagctgt	gaagtgtggt	aaaatgtggt	ttgatacagt	aatatataaa											1144	
tatgtctata	tatatgagga	acttgtggtt	tttaaattggt	ggccaggtag	aggaactaga											1204	
aaagagattt	tgttgccgtg	tttctgacca	tctgtgttat	tgctactgag	aaactaaaat											1264	
agtaaattta	ctaaaactac	actgcaccat	gtagtaata	aacagatctg	ccttaaagaa											1324	
aagaaaattt	tagaaagaaa	tattgttgct	cagtgttggt	aatatagctc	aagaattgag											1384	
tttatatttg	cagtatgcta	taaatgatac	ccccctacca	caccacaca	cacagttttt											1444	
gtctaatagaa	aatgttgctg	tgattattta	taattggtag	tatttcttcc	agaagaagct											1504	
aaaataagac	tggcacttac	cctgaagtgc	attaataaaa	ccacacttta	aaatta											1560	

B

<210> 6
<211> 311
<212> PRT
<213> HUMAN

<400> 6

Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
1 5 10 15

Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
20 25 30

Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
35 40 45

Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60

Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80

Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95

Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
100 105 110

Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
115 120 125

Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
130 135 140

Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
145 150 155 160

Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
165 170 175

Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
180 185 190

Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
195 200 205

Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
210 215 220

Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
225 230 235 240

Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
245 250 255

His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
260 265 270

: His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
275 280 285

' Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
290 295 300

Lys Val Lys Leu Gly Asn Pro
305 310

B